

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/522,991

CRF Edit Date: 2-11-05  
Edited by: KE

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

 Deleted: invalid beginning/end-of-file text; \_\_\_ page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

\_\_\_ Other:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,991

DATE: 02/11/2005

TIME: 16:11:15

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02112005\J522991.raw

3 <110> APPLICANT: Hitachi High-Technologies Corporation  
 5 <120> TITLE OF INVENTION: A method of detecting a nucleic acid using DNA  
 6 microarray and a nucleic acid detecting apparatus  
 8 <130> FILE REFERENCE: PH-1503-PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,991  
 C--> 10 <141> CURRENT FILING DATE: 2005-02-02  
 10 <160> NUMBER OF SEQ ID NOS: 4  
 12 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply  
 Corrected Diskette Needed

(PS.1)

## ERRORED SEQUENCES

47 <210> SEQ ID NO: 4  
 48 <211> LENGTH: 50  
 49 <212> TYPE: DNA  
 50 <213> ORGANISM: Artificial Sequence  
 52 <220> FEATURE:  
 53 <223> OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA  
 55 <400> SEQUENCE: 4  
 56 tcctctaatt ccaggatcaa caacaaccag aggttttgca tggccccgta 50  
 E--> 62 1/2  
 E--> 63 dsmdb.1878912.1

deleted

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/522,991

DATE: 02/11/2005

TIME: 16:11:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02112005\J522991.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:51 SEQ:4  
L:62 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
M:254 Repeated in SeqNo=4  
L:63 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9 ✓  
L:63 M:112 C: (48) String data converted to lower case,  
L:63 M:252 E: No. of Seq. differs, <211> LENGTH:Input:50 Found:58 SEQ:4 ✓